Figure 16: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mi1.1   3768 bp
Sequence 2: Mi1.2   3774 bp
Sequence 3: Rpi-blb2   3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 89
Sequences (2:3) Aligned. Score: 89
Guide tree   file created: [/ebi/extserv/clustalw-work/interactive/clustalw-
20040503-14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2   Score:68908
Group 2: Sequences: 3   Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created   [/ebi/extserv/clustalw-work/interactive/clustalw-
20040503-14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

```
Mi1.1       ATGGAAAAACGAAAAGATAATGAAGAAGCAAACAACTCATTGGTGCTATTTCTGCTCTT   60
Mi1.2       ATGGAAAAACGAAAAGATATTGAAGAAGCAAACAACTCATTGGTGTTATTTCTGCTCTT   60
Rpi-blb2    ATGGAAAAACGAAAAGATAATGAAGAAGCAAACAACTCATTGGAGTCATTTCTGCTCTT   60
            ******************** * *************************** *  *************
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Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Mi1.1     AGCAAGGACACATTGCCGATGTTCTGGTTTCCTAGAGA-------ATGAGGAAAATCAA   111
Mi1.2     AGCAAGGACACATTGCCAATGTTCTAATTTCCTAGAGA-------ATGAGGAAAATCAA   111
Rpi-blb2  CGCAAGGATGCTGCCAATGTTCTGGATTCCTAGAGAGATTAAAGAATGAAGAAGATCAA   120
          *******  *** ******      *  *  ***** **  **** *** ******


Mi1.1     AAAGCTCTTGACAAAGATCAAGTTGAAAAGATAAAATTGAAAAATGGCATTTATTTGTACA   171
Mi1.2     AAAGCTCTTGACAAAGATCAAGTTGAAAAGCTAAAAATGAAAAATGGCATTTATTTGTACA   171
Rpi-blb2  AAGGCTGTTGATGTGGATCTGATTGGGAAGAAGTTGAAAATTGAAGCTGACATTTATTTGTACA   180
          ** *** ****  ****   *  ******   *  ***************


Mi1.1     TATGTTCAGCTTTCTTGTTCCGATTTGAGCAGTTTGAAGATATAATGACTAGAAAAAGA   231
Mi1.2     TATGTTCAGCTTTCTTATTCCGATTTGAGCAGTTTGAAGATATAATGACTAGAAAATAGA   231
Rpi-blb2  TATGTCCAGCTTTCTTATTCCGATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGA   240
          ***** ***********  ********  *** *******************  ***


Mi1.1     CAAGAGGTTGAGAATCTGCTTCAACCACTTTTGGATGATGATG---------------   274
Mi1.2     CAAGAGGTTGAGAATCTGCTTCAATCACTTTTGGATGATGATG---------------   274
Rpi-blb2  CAAGAGGTTGAGAATCTGCTTCAACCAATTTGGATGATGATGGCAAAGACGTCGGGTGT   300
          ************************  **   ****************


Mi1.1     ------TCTTTACTAGCCTCACCAGTAATATGGATGACTGTATCAGCTTGTATCATCGT   327
Mi1.2     ------TCCTTACTAGCCTCACCAGTAATATGGATGACTGTATCAGCTTGTATCATCGT   327
Rpi-blb2  AAATATGTCCTTACTAGCCTCGCCGGTAATATGGATGACTGTATAAGCTTGTATCATCGT   360
          **  ************* ** *****************   ***************


Mi1.1     TCTTATAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCTCTCTTGAATCTC   387
Mi1.2     TCTTATAAATCAGATGCCATCATGATGATGATGAGCAATTGGACTTCCTCTCTTGAATCTG   387
Rpi-blb2  TCT--AAATCAGATGCCACCATGATGGATGAGCAATTGGGCTTCCTCTCTTGAATCTC   417
          ***  ***********  ***********************  ***********
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33

Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Mi1.1     TATCATCTATCCAAGCATCACGCTGAAAAGAGATATTTCCTGGAGTGACTCAATATGAAGTT  447
Mi1.2     TATCATCTATCCAAGCATCACGCTGAAAAGAGATATTTCCTGGAGTGACTCAATATGAAGTT  447
Rpi-blb2  TCTCATCTATCCAAGCATCACGCTGCTGCTGAAAAGATGTTTCCTGGAGTGACTCAATATGAGGTT  477
          * ********** ********************** ***

Mi1.1     CTTCAGAATATATGTGGCAACATAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT  507
Mi1.2     CTTCAGAATGTATGTGGCAACATAAGAGATTTCCATGGGTTGATACTGAATGGTTGCATT  507
Rpi-blb2  CTTCAGAATGTATGTGGCAACATAAGAGATTTCCATGGATTGATAGTGAATGTTGCATT  537
          ********* ***************************** ******* ****** ********

Mi1.1     AAGCATGAGAGATGGTTGAGAAATGTCTTRCCTCTGTTTCAACTCATGGCTGACAGAGTAGGA  567
Mi1.2     AAGCATGAGAGATGGTTGAGAAATGTCTTACCTCTGTTTCAACTCATGGCTGAAAGAGAGTAGGA  567
Rpi-blb2  AAGCATGAGAGATGGTTGAGAAATGTCTTATCTCTGTTTCAACTGATGGCTGAGAGAGTAGGA  597
          *********************************  ********** ******** ******** *

Mi1.1     CACTTCCTTTGGGATGATCAGACTGATGAAGACTCTCGACTCTCCGAGCTAGATGAGGAT  627
Mi1.2     CACTTCCTTTGGGAGGATCAGACTGATGAAGACTCTCGGCTCTCCGAGCTAGATGAGGAT  627
Rpi-blb2  CGCTTCCTTTGGGAGGATCAGGCTCAGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGAT  657
          * ***********  *******  ***** ****************** ***************

Mi1.1     GAACAAAAATGATAGAGACTCTCTGACTTTTCAAGCTAGCACATCTACTCTTGAAGATCGTT  687
Mi1.2     GAACACAATGATAGAGACTCTCTGACTCTTCCAGCTAACACATCTACTCTTGAAGATTGTT  687
Rpi-blb2  GATCAGAATGATAAAGACCCCTCAACTCTTCAAGCTAGCACATCTACTCTTGAAGATTGTT  717
          ** ** ******** *** ** ***** *** *** ***************** ***

Mi1.1     CCGGTTGAACTGGAGGTTATACACATGTTATACAAACTTGAAAGCTTCAACTTCAGCT  747
Mi1.2     CCAACTGAACTGGAGGTTATGCACATATGTTATACAAATTTGAAAGCTTCAACTTCAGCA  747
Rpi-blb2  CCAACTGAATTGGAGGTTATGCACATATGTTATAAAACTTTGAAAGCTTCAACTTCAACA  777
          **  **** ********** ********** ** ********* *

Mi1.1     GAAGTTGGACTCTTCATTAAGCAGCTTCTAGAAAACCTCTCCAGATATTCTGAGGGAATAT  807
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34

Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Mi1.2       GAAGTTGGACGCGCTTCATTAAGAAGCTCCTGGAAACCTCACCGGATATTCTCAGAGAATAT   807
Rpi-blb2    GAAATTGGACGCGCTTCATTAAGAAGCTCCTGGAAACCTCCTCCGGACATTCTCAGAGAATAT   837
            *** ****** ******************** ** ****** ** ******* **

Mi1.1       CTAATTCCTCTGCAAGAGCACACATGGTAACTGTTATTACCCCTAGCACTTCAGGGGCTCGA   867
Mi1.2       ATCATTCAACTACAAGAGCACATATGTTAACTGTTAACTGTTAACTGTTTAGGGGGCTCGA   867
Rpi-blb2    CTGATTCATCTACAAGAGCACATATGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGA   897
            * **** ** ********** *** ********** ***** **********

Mi1.1       AACATTCATGTCATGATGGAATTCCTATTACTTATTCTTTCTGATATGCC---CAAGGAC   924
Mi1.2       AACATTCATGTCATGATGGAATTCCTATTACTTATTCTTTCTGATATGCC---CAAGGAC   924
Rpi-blb2    AACATTCATGTCATGATGGAATTCCTATTACTTGATTATTCTTTCTGATATGCCGCCCAAGGAC   957
            ********************************* *******

Mi1.1       TTTATTCATCATGACAAACTTTTTGATCTCTTGGATCGTGTCGGAGTACTTACCAGGGAG   984
Mi1.2       TTTATTCATCATGACAAACTTTTTGATCTCTTGGCTCATGTTGGAACACTTACCAGGGAG   984
Rpi-blb2    TTTATTCATCATGACAAACTTTTTGATCTCTTGGCTCGTGTTGTGGTAGCACTTACCAGGGAG   1017
            ********************************** ** ** * ***************

Mi1.1       GTATCAACTCTTGTACGTGACTTGGAAGAGGAACCAAGGAATAAAGAGGGTAATAACCAA   1044
Mi1.2       GTATCGACTCTTGTACGTGACTTGGAAGAGAGAGAGAAATTAAGGAGAATAAAGAGGGTAATAACCAA   1044
Rpi-blb2    GTATCAACTCTTGTACGCGACTTGGAAGAGAGAGAGAAATTAAGGAGAGTACTGACGAA   1077
            ***** *********** ************ ** * *** ***** *** * ** * **

Mi1.1       ACAAATTGTGCAACCCTAGACTTGCTGGAAAAATATTGAACTCCTCAAGAAAGATCTCAAA   1104
Mi1.2       ACAAATTGTGCAACCCTAGACTTGCTGGAAAAATATTGAACTCCTCAAGAAAGATCTCAAA   1104
Rpi-blb2    ACAAATTGTGCAACCCTAAAGTTTCTGGAAAAATATTGAACTCCTTAAGGAAGATCTCAAA   1137
            ****************** * ** ******* *** ********* *** *********

Mi1.1       CATGTTTATCTGAAAGCCCCTGGATTCATCTCAATGTTGCTTCCCCATGAGTGATGGACCA   1164
Mi1.2       CATGTTTATCTGAAAGCCCCCAAATTCATCTCAATGTTGCTTCCCCATGAGTGATGGACCA   1164
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35

Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Rpi-blb2    CATGTTTATCTGAAAGTCCCGGATTCATCTCAATATTGCTTCCCCATGAGTGATGGACCT  1197
                            ************** **  ***********************

Mi1.1       CTCTTCATGCATCTTCTACACATACACTTAAATGATTGTTAGATTCTTAATGCTTATTCA  1224
Mi1.2       CTCTTCATGCATCTTCTACACATACACTTAAATGATTGTTAGATTCTTAATGCTTATTCA  1224
Rpi-blb2    CTCTTCATGCATCTGCTACAGAGACACTTAGATGATGATTTGCTTGCTGGATTCCAATGCTTATTCA  1257
            ************** ****** *  ****** * ***** ***********

Mi1.1       ATTGCTTTGATAAAGGAAGAAATCGAGCTGGTGAAGCAAGACCTGAAATTCATAAGATCA  1284
Mi1.2       ATTTCTTTGATAAAGGAAGAAATCGAGTTGGTGAGTTGGTGAGTCAAGAACTGGAATTCATAAGATCA  1284
Rpi-blb2    ATTGCTTTGATAAAGGAACAAATTGGGCTGGTGAAAGAAGACTTGGAATTCATAAGATCT  1317
            *** ************** **** *  ****** ****  ** **************

Mi1.1       TTCTTTGTGGATGCTG---AGCAAGGATTGTATAAAGATCTCTGGGCACGTGTTCTAGAT  1341
Mi1.2       TTCTTTGGGGATGCTGCTGCTGAGCAAGGATTGTATAAAGATATCTGGGCACGTGTTCTAGAT  1344
Rpi-blb2    TTTTTCGCGAATATTG---AGCAAGGATTGTATAAAGATCTCTGGGAACGTGTTCTAGAT  1374
            ** ** * * **   **   *************************** ******* *********

Mi1.1       GTGGCTTATGAGGCAAAAGATGTCATAGATTCAATTATTGTTCGAGATAATGGTCTCTTA  1401
Mi1.2       GTGGCTTATGAGGCAAAAGATGTCATAGATTCAATTATTGTTCGAGATAATGGTCTCTTA  1404
Rpi-blb2    GTGGCATATGAGGCAAAAGATGTCATAGATTCAATTATTGTTCGAGATAATGGTCTCTTA  1434
            ***** ******************************************************

Mi1.1       CATCTTATTTCTCACTTCCCATTCCCATTACCATAAAGGAAGATCAAAACTTATCAAAGAAGAGATC  1461
Mi1.2       CATCTTATTTCTCACTTCCCATTCCCATTACCATAAAGGAAGATCAAAACTTATCAAAGAAGAGATC  1464
Rpi-blb2    CATCTTATTTCTCACTTCCCATTCCCATTACCAGAAAGGAAGATGATGCTTATCAAAGAAGAGGTC  1494
            ***** ********************************* *  ************************ **

Mi1.1       TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACTCTCCCAAG  1521
Mi1.2       TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACTCTCCCAAG  1524
Rpi-blb2    TCTGATTTACATGAGAACAGAACAGAACATTTCCAAGAACAGAGAACAGAGGTCTCATCGTTGTGAACTCTCCCAAG  1554
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Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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                  **** ***** ********** ***** ********** ******************
Mi1.1     AAACCAGTTGAGAGAAAGTCATTGACAACTGATAAATAACTGTAGGTTTGAGGAGGAA  1581
Mi1.2     AAACCAGTTGAGAGAAAGTCATTGACAACTGATAAATAATTGTAGGTTTGAGGAGGAG  1584
Rpi-blb2  AAACCAGTTGAGAGCAAGTCATTGACAACTGATAAATAATTGTAGGTTTGGTGAGGAG  1614
                  ************** ********************************** *****

Mi1.1     ACAAACTTGATACTTAGAAAGCTCACCAGTGGATCGGCAGATCTAGATGTCATTTCGATC  1641
Mi1.2     ACAAACTTGATACTTAGAAAGCTCACCAGTGGACCCGCAGATTTAGATGTCATTTCGATC  1644
Rpi-blb2  ACAAACTTGATACTTAGAAAGCTCACCAGTGGACCGGCAGATCTAGATGTCATTTCGATC  1674
                  *********************************** * ********************

Mi1.1     ACTGGTATGCCGGGTTCAGGTAAAACTACTTTGGCATACAAAGTATACAATGATAAGTCA  1701
Mi1.2     ACCGGTATGCCGGGTTCAGGTAAAACTACTTTGGCATACAAAGTATACAATGATAAGTCA  1704
Rpi-blb2  ATTGGTATGCCGGGTTTAGGTAAAACTACTTTGGCGTACAAAGTATACAATGATAAATCA  1734
                  *  ************* ****************** * *******************  ***

Mi1.1     GTTTCTAGCCGTTCGACCTTCGTGCATGGTGCACGGTCGCGACCAAGGATGTGATGAGAAG  1761
Mi1.2     GTTTCTAGACATTTGACCTTCGTGCATGGTGCACGGTCGCGACGGTCGATCAAGGATGACAAG  1764
Rpi-blb2  GTTTCTAGCCATTCGACCTTCGTGCATGGTGCACGGTCGCGACCAAGTATATGACGAGAAG  1794
                  ******** * **** ************************** ** ** *** ****

Mi1.1     AAGTTGTTGAATACAATTTTCAGTCAAGTTAGTGACTCAGATTCAAAATTGAGTGAGAAT  1821
Mi1.2     AAGTTGTTGGATACAATTTCAGTCAAGTTAGTGGCTCAGATTCAAATTGAGTGAGAAT  1824
Rpi-blb2  AAGTTGTTGGATAAAATTTTCAATCAAGTTAGTGACTCAAATTCAAAATTGAGTGAGAAT  1854
                  ********* *** **** * ********* **** ********* ************

Mi1.1     ATTGATGTTGCTGATAAATTACGGAAACAACTGTTTGGAAAGAGGTATCTTATTGTCTTA  1881
Mi1.2     ATTGATGTTGCTGATAAATTGCGGAAACAACTGTTTGGAAAGAGGTATCTTATTGTCTTA  1884
Rpi-blb2  ATTGATGTTGCTGATAAAACTACGGAAACAATTGTTTGGAAAGAGGTATCTTATTGTCTTA  1914
                  ****************** * ********* ** **************************
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37

Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Mi1.1       GATGACGTGTGGGATACTACTACACATGGGATGAGTTAACAAGACCTTTCCTGAATCTAAG  1941
Mi1.2       GATGATGTGTGGGATACTACTACACATGGGATGAGTGAGTTGACAAGACCTTTCCTGAAGCTAAG  1944
Rpi-blb2    GATGACGTGTGGGATACTAATACATGGGATGAGCTAACAAGACCTTTCCTGATGGTATG  1974
            ***** *********** ***** **** *** ******* **
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Mi1.1       AAAGGAAGTAGGATTATTTGACAACTCGGGAAAAGGAAGTGGCTTTGCATGGAAAGCTG  2001
Mi1.2       AAAGGAAGTAGGATTATTTGACAACTCGAGAAAGGAAGTGGCTTTGCATGGAAAGCTG  2004
Rpi-blb2    AAAGGAAGTAGAATTATTTGACAACTCGAGAATCGAGAAAGAAAGAAAGTTGCTTTGCATGGAAAGCTC  2034
            ********** ***** ******** ** ****** *** ***************
```

```
Mi1.1       AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTGGGAACTATTAGAG  2061
Mi1.2       AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTGGGAACTTTTAGAT  2064
Rpi-blb2    TACACTGATCCCTTTAACCTTCGATTGCTAAGATCAGAAGAAGAAAGTTGGGAGTTATTAGAG  2094
            ********** *** * ****************** * ***** ***** * *****
```

```
Mi1.1       AAAAGGGCATTTGGGAATGAGAGTTGCCCTGATGAACTATTAGATGTCGGTAAAGAAATA  2121
Mi1.2       AAAAGGACATTTGGTAATGAGAGTTGCCCTGATGAACTATTAGATGTCGGTAAAGAAATA  2124
Rpi-blb2    AAAAGGGCATTTGGGAAACGAGAGTTGCCCTGATGAACTATTGGATGTTGGATAAAGAAATA  2154
            ****** ******* ** ** ****************** ***** * *** ************
```

```
Mi1.1       GCCGAAAAATTGTAAAGGGCTTCCTTGGTGGCTGATCTGATTGCTGGAGTCATTGCTGGG  2181
Mi1.2       GCCGAAAATTGTAAAGGGCTTCCTTGGTGGCTGATCTGATTGCTGGAGTCATTGCTGGG  2184
Rpi-blb2    GCCGAAAATTGTAAAGGGCTTCCTTGGTGGCTGATCTGATTGCTGGAATCATTGCTGGG  2214
            ******* ****** ****************************** ************
```

```
Mi1.1       AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTTCTTTTATTTTG  2241
Mi1.2       AGGGAAAAGAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTTCTTTTATTTTG  2244
Rpi-blb2    AGGGAAAAGAAAAGAGTGTGTGGCTTGAAGTTGTAAATAATTGTAAATAATTTGTATTTCCTTTATTTTG  2274
            ************* *************** ** ** ***** *** *********
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38

Docket No.: 13477-00002-US

Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

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Mi1.1       AACAGTGAAGTGGAAGTGATGAAAGTTATAGAATTAAGTTATGACCATTTACCACATCAC   2301
Mi1.2       AACAGTGAAGTGGAAGTGATGAAAGTTATAGAATTAAGTTATGACCATTTACCACATCAC   2304
Rpi-blb2    AAGAATGAAGTGGAAGTGATGAAAGTTATAGAAATAAGTTATGACCACTTACCTGATCAC   2334
            ** * ******************** ******************** ***** *****

Mi1.1       CTCAAGCCATGCTTGCTGTATTTGCAAGTTTCCGAAGGACACTTCATTGACAATCTAT    2361
Mi1.2       CTCAAGCCATGCTTGCTTCACTTTGCAAGTGGCCGAAGGACACTCCTTTGACAATCTAT    2364
Rpi-blb2    CTGAAGCCATGCTTGCTTCTGTACTTGCAAGTGCGCGCCGAAGGACTGGTAACGACAATCCAT   2394
            ** *************** * * ********* * *** ** **

Mi1.1       GAGTTGAAATGTTTATTCGGTGCTGAAGGATTTGTGGGAAAGACGGAGATGAACAGTATG   2421
Mi1.2       TTGTTTACTGTTTATTTGGGGTGCTGAAGGATTTGTGGGAAAGACGGAGATGAAGGGTATA   2424
Rpi-blb2    GAGTTGAAACTTATTGGGGGTTTGAAGGATTTGTGGGAAAAGACAGAGTCTG    2454
            *** *   **   **   ***   ***************** ******* ** ****** ** *

Mi1.1       GAAGAAGTGGTGAAGATTTATATGGATGATTAATTACAGTAGCTTGGTAATTTGTTTC   2481
Mi1.2       GAAGAAGTGGTGAAGATTTATATGGATGATTAATTCCAGTAGCTTGGTAATTTGTTTC   2484
Rpi-blb2    GAAGAAGTGGTGAAAATTTATTTGGATGATTTAATTCCAGTAGCTTGGTAATTTGTTTC   2514
            ************* ***** ******** ********************************

Mi1.1       AATGAGATAGGTTATGCACTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTTTG   2541
Mi1.2       AATGAGATAGGTGATATACTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTTTG   2544
Rpi-blb2    AATGAGATAGGTGATTATTACCCTACTTGCCAACTTCATGATCTTGTGCATGACTTTTGTTTC   2574
            ************* **  *  *  * **** ************************

Mi1.1       ATAAAAGCAAGAAAGGAAAATTTGTTTGATCAGATAAGATCAAGTGCTCCATCAGATTTG   2601
Mi1.2       ATAAAAGCAAGAAAGGAAAATTTGTTTGATCGGATAAGATCAAGTGCTCCATCAGATTTG   2604
Rpi-blb2    ATAAAAGCAAGAAAGGAAAAGTTGTGTGATCGGATAAGTTCAAGTGCTCCATCAGATTTG   2634
            ******************** **** ******* ******* ****************

Mi1.1       TTGCCTCGTCAAATTACCATTGATTGTGATGAGGAGGAG---CACTTTGGGCTTAATTTT   2658
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Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Mi1.2     TTGCCTCGTCAAATTACCATTGATTATGATGAGGAGGAGGAGCACTTTGGGCTTAATTTT  2664
Rpi-blb2  TTGCCACGTCAAATTAGCATTGATTATGATGATGATGAAGAGCACTTTGGGCTTAATTTT  2694
          ***** ********* ** ** ****** ** ***********

Mi1.1     GTCATGTTCGATTCAAATAAGAAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA  2718
Mi1.2     GTCATGTTCGATTCAAATAAGAAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA  2724
Rpi-blb2  GTCCTGTTCGGTTCAAATAAGAAAAAGGCATTCCGGTAAACACCTCTATTCTTTGACCATA  2754
          *** ****** ***************************** ******************* ***

Mi1.1     ATTGGAGACCAGCTGGATGACAGTGTTCTGATGCATTTCACCTAAGACACTTGAGGCTT  2778
Mi1.2     AATGGAGACCAGCTGGATGACAGTGTTCTGATGCATTTCACCTAAGACACTTGAGGCTT  2784
Rpi-blb2  AATGGAGATGAGCTGGACGACCATCTTTCTGATACATTTCATCTAAGACACTTGAGGCTT  2814
          * ******  ********  *   ********* *  ********  *****************

Mi1.1     CTTAGAGTGTTGGACCTGCATACGTCTCTTTATCATGGTGAAAGATTCTTTGCTGAATGAA  2838
Mi1.2     ATTAGAGTGTTGGACCTGGAACCCCTCTTAATCATGGTGAATGGTGAATGATTCTTTGCTGAATGAA  2844
Rpi-blb2  CTTAGAACCTTGCACCTGGAATCCCTCTTTATCATGGTTAAATGGTTAAATGATTCTTTGCTGAATGAA  2874
          *****  *** ******  *  *  ***** * ********************

Mi1.1     ATATGCATGTTGAATCATTTGAGGTACTTATCCATTGACACACAAGTTAAATATCTGCCT  2898
Mi1.2     ATATGCATGTTGAATCATTTGAGGTACTTAAGAATTCGGACACACAAGTTAAATATCTGCCT  2904
Rpi-blb2  ATATGCATGTTGAATCATTTGAGGTACTTAAGCATTGGGACAGAGAAGTTAAATCTCTCTGCCT  2934
          ****************************  ***  *** ********* ********

Mi1.1     TTGTCTTTCTCCAAACCTCTGGAATCTAGAAAGCCTGTTTGTGTCTACCAACAGATCAATC  2958
Mi1.2     TTCTCTTTCTCAAACCTCTGGAATCTAGAAAGCTAGAAAGTCTGTTTGTGTCTAACAAAGGATCAATC  2964
Rpi-blb2  TTGTCTTTCTCAAACCTCTGGAATCTAGAAATCTAGAAATCTTGTTTGTGGATAACAAAGAATCAACC  2994
          ** ******* ***********************  ** ***   ***  ****** *

Mi1.1     TTGGTACTATTACCGAGAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGATGCT  3018
Mi1.2     TTGGTACTATTACCGAGAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGGTGCT  3024
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Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Rpi-blb2    TTGATACTATTACCGAGAATTTGGGGATCTTGTAAAGTTGCAAGTGCTGTTCACGACTGCT  3054
            *** ************************ ********** *  * ****

Mi1.1       TGTTCTTTCTTTGATATGGATGCAGAGATGAATCAATATTGATAGCAGAGGACACAAAGTTA  3078
Mi1.2       TGTTCTTTCTTTGATATGGATGCAGAGATGAATCAATATTGATAGCAGAGGACACAAAGTTA  3084
Rpi-blb2    TGTTCTTTCTTTGATATGGATGCAGAGATGAATCAATACTGATAGCAGAGGACACAAAGTTA  3114
            ************************************* ************************

Mi1.1       GAGAACTTGAGAATATTAACGGAACTGTTGATTTCCTATTCGAAAGATACAAAGAATATT  3138
Mi1.2       GAGAACTTGAGAATATTAGGGGAACTGTTGATTTCCTATTCGAAAGATACAATGAATATT  3144
Rpi-blb2    GAGAACTTGACACAGCATTAGGGGAACTCGTGCTTTCCTATTGGAAAGATACAGAGGATATT  3174
            ********** *  **** * **  ******* ** *********** * *****

Mi1.1       TTCAAAAGGTTTCCCAATCTTCAGTTGCTTTCATTGAACTCAAGGAGTCATGGGATTAT  3198
Mi1.2       TTCAAAAGGTTTCCCAATCTTCAGTTGCTTTCAGTTGAACTCAAGGAGTCATGGGATTAT  3204
Rpi-blb2    TTCAAAAGGCTTCCCAATCTTCAAGTGCTTTCAAACTCAAGGAGTCATGGGATTAT  3234
            ********* ************* ** **** ** *****************

Mi1.1       TCAACAGAGCAACATTGGTTCTCGGAATTGGATTCCTAACTGAACTAGAAACACTCTCT  3258
Mi1.2       TCAACAGAGCAACATTGGTTCCCGAAATTGGATTGCCTAACTGAACTAGAAACACTCTGT  3264
Rpi-blb2    TCAACAGAGCAATATTGGTTCCCGAAATTGGATTCCTAACTGAACTAGAAAAACTCACT  3294
            ************ ******** ** ********** ********************* **** *

Mi1.1       GTAGGTTTTAAAAGTTCAAAACACAAAACGATAGTGGGTCCTCTGTAGCGACAAATCGGCCG  3318
Mi1.2       GTAGGTTTTAAAAGTTCAAAACACAAAACCACTGGGTCCTCTGTTGTGACAAATCGGCCG  3324
Rpi-blb2    GTAGATTTGAAAGATCAAACACAAAACACAAATGACAGTGGGTCCTCTGCAGCCATAAATCGGCCA  3354
            **** ***** ** *** *********** *  * *********

Mi1.1       TGGGATTTTCACTTCCCTTCAAATTTGAAAATACTGTGGTTGCGTGAATTTCCGCTGACA  3378
Mi1.2       TGGGATTTTCACTTCCCTTCCCTTCAAATTTGAAAGAACTGTTGTTGTATGACTTTCCTCTGACA  3384
Rpi-blb2    TGGGATTTTCACTTTCCTTCCCTTCCTTCGAGTTTGAAAAAGATTGCAATTGCATGAATTTCCTCTGACA  3414
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Application No.: 10/567,980
Amendment dated October 24, 2007
Reply to Office Action of April 24, 2007
Replacement Sheets

Docket No.: 13477-00002-US

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Mil.1      TCCGATTCACTACTATCAACAATAGCGAGACTGCCCAACCTTGAAGAGTTGTCCCTTATCAT  3438
Mil.2      TCCGATTCACTACTATCAACAATAGCGAGACTGCCCAACCTTGAAAATTGTCCCTTTATGAT  3444
Rpi-blb2   TCCGATTCACTACTATCAACAATAGCGAGACTGCTGAACCTTGAAGAGTTGTACCTTTATCGT  3474
           ******************************* *  **** ******* *

Mil.1      ACAATCATCCATGGAGAAGAGAATGGAACATGGGGGAGGAAGACACCTTTGAGAATCTCAAA  3498
Mil.2      ACAATCATCCAGGGAGGAGAAGAATGGAACATGGGGGAGGAAGACACTTTTGAGAATCTCAAA  3504
Rpi-blb2   ACAATCATCCATGGGGAAGAATGGAACATGGGGGAGGAAGAAGACACCTTTGAGAATCTCAAA  3534
           ********** **  ***************** ** ******************

Mil.1      TTTTTGAACTTCAATCAAGTTAGTATTTCCAAGTGGGAGGTTGGAGAGGAATCCTTCCCC  3558
Mil.2      TTTTTGAACTTGCGTCTACTGGACTCTTTCCAAGTGGGAGGTTGGAGAGGAATCCTTCCCC  3564
Rpi-blb2   TGTTTGATGTTGAGTCAAGTGATTCTTTCCAAGTGGGAGGTTGGAGAGGAATCTTTCCCC  3594
           * ***** **   **  * * ************************** ** ***

Mil.1      AATCTTGAGAAATTAAAAACTGCGGGATGTCATAAGCTAGAGGAGATTCCACCTAGTTTT  3618
Mil.2      AATCTTGAGAAATTAAAACTAAAAACTGGTGGTAAGCTTGAGGAGATTCCACCTAGTTTT  3624
Rpi-blb2   ACGCTTGAGAAATTTATTCCTGACTGTCGGACTGTCATAAATCTTGAGGAGATTCCGTCTAGTTTT  3654
           *  ********** ***  *** ** ** ** ************  ********

Mil.1      GGAGATATTTATTCATTGAAATCTATCAAAATTGTAAAGAGTCCTCAACTTGAAGATTCT  3678
Mil.2      GGAGATATTTATTCATTGAAATTTATCAAAATTTATCAAAATTATCAAACTTGAAGATTCT  3684
Rpi-blb2   GGGGATATTTATTCATTGAAAAATTATCGAACTTGTAAGGAGCCCTCAACTTGAAAATTCC  3714
           ** ********** ******  ****** *** ** ************** ****

Mil.1      GCTCTCAAAATTAAGGAATACGCTGAAGAGATATGAGGGGGAGGGGACGAGCTTCAGATCCTT  3738
Mil.2      GCTCTCAAGATTAAGAAATACGCTGAAGAGATATGAGGGGGAGGGGACGAACGATCTTCAGATCCTT  3744
Rpi-blb2   GCTCTCAAGATTAAGGAATATGCTGAAGATATGCTGAAGATATGAGGGGGACGAGCTTCAGATCCTT  3774
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Application No.: 10/567,980

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Mil.1      GGCCAAAAGAATATCCCCTTATTTAAGTAG  3768
Mil.2      GGCCAGAAGAATATCCCCTTATTTAAGTAG  3774
Rpi-blb2   GGCCAGAAGGATATCCCGTTATTTAAGTAG  3804
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